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 Hilight option is not available in file(s) 398, 399  
 HILIGHT set on as '%'  
     132189 NEISSERIA  
     59916 MENINGITIDIS  
 S1 57166 NEISSERIA (1W) MENINGITIDIS  
 ? s s1 and fur (1w) gene  
 Processing  
 Processed 10 of 60 files ...  
 Processing  
 Processed 40 of 60 files ...  
 Completed processing all files  
     57166 S1  
     1108021 FUR  
     8745398 GENE  
     1647 FUR(1W)GENE  
 S2 60 S1 AND FUR (1W) GENE  
 ? rd  
 >>>Duplicate detection is not supported for File 398.  
 >>>Duplicate detection is not supported for File 654.  
 >>>Duplicate detection is not supported for File 349.  
 >>>Duplicate detection is not supported for File 348.  
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 >>>Duplicate detection is not supported for File 174.  
 >>>Duplicate detection is not supported for File 447.  
 >>>Duplicate detection is not supported for File 345.  
 >>>Duplicate detection is not supported for File 342.  
 >>>Duplicate detection is not supported for File 761.  
 >>>Duplicate detection is not supported for File 70.  
 >>>Duplicate detection is not supported for File 128.  
 >>>Duplicate detection is not supported for File 449.  
 >>>Duplicate detection is not supported for File 107.  
 >>>Duplicate detection is not supported for File 286.  
 >>>Duplicate detection is not supported for File 446.  
 >>>Duplicate detection is not supported for File 429.  
 >>>Duplicate detection is not supported for File 459.  
 >>>Duplicate detection is not supported for File 229.  
  
 >>>Records from unsupported files will be retained in the RD set.  
 >>>Record 440:10925408 ignored; incomplete bibliographic data, not retained  
     in RD set  
 >>>Record 440:5352096 ignored; incomplete bibliographic data, not retained  
     in RD set  
 >>>Record 440:4304990 ignored; incomplete bibliographic data, not retained  
     in RD set  
 >>>Record 440:3535442 ignored; incomplete bibliographic data, not retained  
     in RD set  
 ...examined 50 records (50)  
 ...completed examining records  
     S3 39 RD (unique items)  
 ? t s3/3,ab/1-39  
 >>>No matching display code(s) found in file(s): 65, 107, 128-129, 135,  
     229, 342, 345, 398, 429, 446-447, 449, 459, 761  
  
 3/3,AB/1 (Item 1 from file: 73)  
 DIALOG(R)File 73:EMBASE  
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12305539 EMBASE No: 2003411326

The iron-responsive regulator Fur is transcriptionally autoregulated and not essential in %Neisseria% %meningitidis%

Delany I.; Ieva R.; Alaimo C.; Rappuoli R.; Scarlato V.

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Journal of Bacteriology ( J. BACTERIOL. ) (United States) 2003, 185/20

(6032-6041)

CODEN: JOBAA ISSN: 0021-9193

DOCUMENT TYPE: Journal ; Article

*after  
57166*

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
NUMBER OF REFERENCES: 39

Fur is a well-known iron-responsive repressor of gene transcription, which is used by many bacteria to respond to the low-iron environment that pathogens encounter during infection. The *%fur% %gene%* in *%Neisseria% %meningitidis%* has been described as an essential gene that may regulate a broad array of genes. We succeeded in obtaining an *N. meningitidis* mutant with the *%fur% %gene%* knocked out and used it to undertake studies of fur-mediated iron regulation. We show that expression of both Fur and the transferrin binding protein Tbp2 is iron regulated and demonstrate that this regulation is Fur mediated for the Tbp2 protein. Footprinting analysis revealed that Fur binds to two distinct sites upstream of its coding region with different affinities and that these binding sites overlap two promoters that differentially control transcription of the *%fur% %gene%* in response to iron. The presence of two independently regulated fur promoters may allow meningococcus to fine-tune expression of this regulator controlling iron homeostasis, possibly during infection.

3/3,AB/2 (Item 2 from file: 73)  
DIALOG(R)File 73:EMBASE  
(c) 2004 Elsevier Science B.V. All rts. reserv.

05724381 EMBASE No: 1994118985

Cloning and sequence analysis of the *%fur% %gene%* encoding an iron-regulatory protein of *%Neisseria% %meningitidis%*  
Karkhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.  
Depart. Microbiol./Infectect. Dis., Univ. Calgary Hlth Sciences Center,  
3330 Hospital Drive N.W., Calgary, Alta. T2N 4N1 Canada  
Gene ( GENE ) (Netherlands) 1994, 141/1 (139-140)  
CODEN: GENED ISSN: 0378-1119  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The *%fur% %gene%*, encoding an iron-regulatory protein in *%Neisseria% %meningitidis%* strain B16B6, has been cloned and sequenced. Its product showed a high degree of homology to known Fur sequences.

3/3,AB/3 (Item 1 from file: 440)  
DIALOG(R)File 440:Current Contents Search(R)  
(c) 2004 Inst for Sci Info. All rts. reserv.

16922452 Document Delivery Available: 000185244400017 References: 31  
TITLE: Molecular cloning and characterization of a 79-kDa iron-repressible outer-membrane protein of *Moraxella bovis*  
AUTHOR(S): Kakuda T (REPRINT); Oishi D; Tsubaki S; Takai S  
AUTHOR(S) E-MAIL: kakuda@vmas.kitasato-u.ac.jp  
CORPORATE SOURCE: Kitasato Univ, Dept Anim Hyg, /Towada/Aomori  
0348628/Japan/ (REPRINT); Kitasato Univ, Dept Anim Hyg, /Towada/Aomori  
0348628/Japan/  
PUBLICATION TYPE: JOURNAL  
PUBLICATION: FEMS MICROBIOLOGY LETTERS, 2003, V225, N2 (AUG 29), P279-284  
GENUINE ARTICLE#: 720CR  
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS  
ISSN: 0378-1097  
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: *Moraxella bovis* expresses an iron-repressible 79-kDa outer-membrane protein, lrpA. DNA and N-terminal amino acid sequence analysis indicate that lrpA is closely related to FrpB of *%Neisseria% %meningitidis%*, FetA of *Neisseria gonorrhoeae* and CopB of *Moraxella catarrhalis*. The results of manganese mutagenesis and a gel-shift assay suggested that the transcription of lrpA is negatively regulated by the ferric uptake regulator. The insertion of an antibiotic resistance cassette into the lrpA gene affected the strain's ability to utilize bovine transferrin and lactoferrin. lrpA was detected in geographically diverse clinical isolates, and the antigenicity of lrpA was conserved in all the

isolates tested. Therefore, *lrpA* may have potential as a candidate vaccine.  
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Elsevier B.V. All rights reserved.

3/3,AB/4 (Item 2 from file: 440)  
DIALOG(R) File 440:Current Contents Search(R)  
(c) 2004 Inst for Sci Info. All rts. reserv.

10591078 References: 37

TITLE: Genetic characterization of wild-type and mutant *fur* genes of  
*Bordetella avium*

AUTHOR(S): Murphy ER; Dickenson A; Militello KT; Connell TD (REPRINT)

AUTHOR(S) E-MAIL: connell@acsu.buffalo.edu

CORPORATE SOURCE: SUNY Buffalo, Sch Med & Biomed Sci, 3435 Main St, 138

Farber Hall/Bufalo//NY/14214 (REPRINT); SUNY Buffalo, Sch Med & Biomed  
Sci, /Bufalo//NY/14214; SUNY Buffalo, Sch Med & Biomed Sci,  
/Bufalo//NY/14214

PUBLICATION TYPE: JOURNAL

PUBLICATION: INFECTION AND IMMUNITY, (1999) V67, N6 (JUN), P3160-3165

GENUINE ARTICLE#: 199GX

PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW,  
WASHINGTON, DC 20005-4171 USA

ISSN: 0019-9567

LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: For most, if not all, organisms, iron (Fe) is an essential element. In response to the nutritional requirement for Fe, bacteria evolved complex systems to acquire the element from the environment. The genes encoding these systems are often coordinately regulated in response to the Fe concentration. Recent investigations revealed that *Bordetella avium*, a respiratory pathogen of birds, expressed a number of Fe-regulated genes (T. D. Connell, A. Dickenson, A. J. Martone, K. T. Militello, M. J. Filiatraut, M. L. Hayman, and J. Pitula, Infect. Immun. 66:3597-3605, 1998). By using manganese selection on an engineered strain of *B. avium* that carried an Fe-regulated alkaline phosphatase reporter gene, a mutant was obtained that was affected in expression of Fe-regulated genes. To determine if Fe-dependent regulation in *B. avium* was mediated by a *%fur%*-like *%gene%*, a fragment of the *B. avium* chromosome, corresponding to the *fur* locus of *B. pertussis*, was cloned by PCR. Sequencing revealed that the fragment from *B. avium* encoded a polypeptide with 92% identity to the Fur protein of *B. pertussis*. In vivo experiments showed that the cloned gene complemented H1780, a *fur* mutant of *Escherichia coli*. Southern hybridizations and PCRs demonstrated that the manganese mutant had a deletion of 2 to 3 Mbp of nucleotide sequence in the region located immediately 5' of the *fur* open reading frame. A spontaneous PCR-derived mutant of the *R. avium* *%fur%* *%gene%* was isolated that encoded a Fur protein in which a histidine was substituted for an arginine at amino acid position 18 (R18H). Genetic analysis showed that the R18H mutant gene when cloned into a low-copy-number vector did not complement the *fur* mutation in H1780. However, the R18H mutant gene was able to complement the *fur* mutation when cloned into a high-copy-number vector. The cloned wild-type *%fur%* *%gene%* will be useful as a genetic tool to identify Fur-regulated genes in the *B. avium* chromosome.

3/3,AB/5 (Item 3 from file: 440)  
DIALOG(R) File 440:Current Contents Search(R)  
(c) 2004 Inst for Sci Info. All rts. reserv.

09909571 References: 64

TITLE: Iron-responsive gene regulation in a *Campylobacter jejuni* *fur* mutant

AUTHOR(S): vanVliet AHM; Wooldridge KG; Ketley JM (REPRINT)

CORPORATE SOURCE: UNIV LEICESTER, DEPT GENET, UNIV RD/LEICESTER LE1

7RH/LEICS/ENGLAND/ (REPRINT); UNIV LEICESTER, DEPT GENET/LEICESTER LE1  
7RH/LEICS/ENGLAND/

PUBLICATION TYPE: JOURNAL

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1998, V180, N20 (OCT), P5291-5298

GENUINE ARTICLE#: 127JD

PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW,  
WASHINGTON, DC 20005-4171  
ISSN: 0021-9193  
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The expression of iron-regulated systems in gram-negative bacteria is generally controlled by the Fur protein, which represses the transcription of iron-regulated promoters by using Fe<sup>2+</sup> as a cofactor. Mutational analysis of the *Campylobacter jejuni* *%fur%* *%gene%* was carried out by generation of a set of mutant copies of *fur* which had a kanamycin or chloramphenicol resistance gene introduced into the regions encoding the N and C termini of the Fur protein. The mutated genes were recombined into the *C. jejuni* NCTC 11168 chromosome, and putative mutants were confirmed by Southern hybridization. *C. jejuni* mutants were obtained only when the resistance genes were transcribed in the same orientation as the *%fur%* *%gene%*. The *C. jejuni* *fur* mutant grew slower than the parental strain. Comparison of protein profiles of fractionated *C. jejuni* cells grown in low- or high-iron medium indicated derepressed expression of three iron-regulated outer membrane proteins with molecular masses of 70, 75, and 80 kDa. Characterization by N-terminal amino acid sequencing showed the 75-kDa protein to be identical to CfrA, a *Campylobacter* coil siderophore receptor homologue, whereas the 70 kDa protein was identified as a new siderophore receptor homologue. Periplasmic fractions contained four derepressed proteins with molecular masses of 19, 29, 32, and 36 kDa. The 19-kDa protein has been previously identified, but its function is unknown. The cytoplasmic fraction contained two iron-repressed and two iron-induced proteins with molecular masses of 26, 55, 31, and 40 kDa, respectively. The two iron-repressed proteins have been previously identified as the oxidative stress defense proteins catalase (KatA) and alkyl hydroperoxide reductase (AhpC). AhpC and KatA were still iron regulated in the *fur* mutant, suggesting the presence of Fur-independent iron regulation. Further analysis of the *C. jejuni* iron and Fur regulons by using two-dimensional gel electrophoresis demonstrated the total number of iron- and Fur-regulated proteins to be lower than for other bacterial pathogens.

3/3,AB/6 (Item 4 from file: 440)  
DIALOG(R)File 440:Current Contents Search(R)  
(c) 2004 Inst for Sci Info. All rts. reserv.

05728818 References: 39

TITLE: IDENTIFICATION, CLONING, AND SEQUENCING OF A GENE REQUIRED FOR  
FERRIC VIBRIOBACTIN UTILIZATION BY *VIBRIO CHOLERAE*

AUTHOR(S): BUTTERTON JR; CALDERWOOD SB (Reprint)

CORPORATE SOURCE: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114  
(Reprint); MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114;

HARVARD UNIV,SCH MED,DEPT MICROBIOL & MOLEC GENET/BOSTON//MA/02115

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N18 (SEP), P5631-5638

GENUINE ARTICLE#: PF222

ISSN: 0021-9193

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Chromosomal DNA downstream of the *Vibrio cholerae* ferric vibriobactin receptor gene, *viuA*, was cloned and sequenced, revealing an 813-bp open reading frame encoding a deduced protein of 271 amino acids. In vitro transcription-translation of this DNA confirmed expression of a protein of the expected size. A deletion mutation of this gene, *viuB*, was created in the classical *V. cholerae* strain O395 by in vivo marker exchange. By cross-feeding studies, this mutant was unable to utilize exogenous ferric vibriobactin but synthesized the siderophore normally; synthesis of siderophore by the mutant was also confirmed by the Arnow assay. Complementation of the mutant with a plasmid encoding only *viuB* restored ferric vibriobactin utilization to normal. Unexpectedly, hydropathicity analysis of *ViuB* did not reveal a signal sequence or transmembrane domain, suggesting that *ViuB* is not a periplasmic or membrane protein but may be a cytoplasmic protein involved in ferric vibriobactin uptake and processing, perhaps analogous to the *Escherichia coli* protein Fes. *ViuB* was not, however, homologous to Fes or to other proteins in the database. Complementation studies revealed that the cloned *V. cholerae* *viuB*

gene could complement an E. coli fes mutant but that the cloned E. coli fes gene could not complement a V. cholerae viuB mutant; Northern (RNA) blot analysis of RNA from wild-type V. cholerae grown in high- and low-iron media revealed a monocistronic viuB message that was negatively regulated by iron at the transcriptional level. The promoter of viuB was located by primer extension and contained a nucleotide sequence highly homologous to the E. coli Fur binding consensus sequence, suggesting that expression of viuB is under the control of the V. cholerae %fur% %gene%.

3/3,AB/7 (Item 5 from file: 440)  
DIALOG(R)File 440:Current Contents Search(R)  
(c) 2004 Inst for Sci Info. All rts. reserv.

05468121 References: 44

TITLE: CHARACTERIZATION OF THE VIBRIO CHOLERAEE OUTER MEMBRANE HEME  
TRANSPORT PROTEIN HUTA - SEQUENCE OF THE GENE, REGULATION OF  
EXPRESSION, AND HOMOLOGY TO THE FAMILY OF TONB-DEPENDENT PROTEINS  
AUTHOR(S): HENDERSON DP; PAYNE SM (Reprint)  
CORPORATE SOURCE: UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712 (Reprint);  
UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712  
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N11 (JUN), P3269-3277  
GENUINE ARTICLE#: NN851  
ISSN: 0021-9193  
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The regulation of hutA, the Vibrio cholerae gene encoding a 77-kDa iron-regulated outer membrane protein required for heme iron utilization, was characterized, and the DNA sequence of the gene was determined. A hutA::Tn5 lac fusion generated previously (D. P. Henderson and S. M. Payne, Mol. Microbiol. 7:461-469, 1993) was transformed into Fur(-) and Fur(+) strains of Escherichia coli and V. cholerae. The results of beta-galactosidase assays on the transformed strains demonstrated that transcription of hutA is regulated by the Fur repressor protein in E. coli and at least partially regulated by Fur in V. cholerae. Analysis of the DNA sequence of hutA indicated that a sequence homologous to the E. coli consensus Fur box was present in the promoter region of hutA. The amino acid sequence of HutA is homologous to those of several TonB-dependent outer membrane proteins. However, when the V. cholerae heme utilization system, which requires one or more genes encoded by the recombinant plasmid pHUT10 in addition to hutA Carried on a second vector, was transferred to a wild-type strain and an isogenic tonB mutant of E. coli, the tonB mutant could utilize heme iron as efficiently as the wild-type strain. These data indicate that the V. cholerae heme utilization system reconstituted in E. coli does not require a functional TonB protein. The tonB mutant transformed with the heme utilization plasmids could not utilize the siderophore ferrichrome as an iron source, indicating that none of the genes encoded on the heme utilization plasmids complements the tonB defect in E. coli. It is possible that a gene(s) encoded by the recombinant heme utilization plasmids encodes a protein serving a TonB-like function in V. cholerae. A region in the carboxy terminus of HutA is homologous to the horse hemoglobin zeta chain, and the amino acids involved in forming the heme pocket in the zeta chain are conserved in HutA. These data suggest that this region of HutA is involved in heme binding.

3/3,AB/8 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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05375535 Genuine Article#: VU635 Number of References: 43  
Title: IDENTIFICATION AND PURIFICATION OF A HEMOGLOBIN-BINDING  
OUTER-MEMBRANE PROTEIN FROM NEISSERIA-GONORRHOEA (Abstract Available)  
Author(s): CHEN CJ; SPARLING PF; LEWIS LA; DYER DW; ELKINS C  
Corporate Source: UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599;  
UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV  
OKLAHOMA,HLTH SCI CTR,DEPT MICROBIOL & IMMUNOL/OKLAHOMA CITY//OK/73190  
Journal: INFECTION AND IMMUNITY, 1996, V64, N12 (DEC), P5008-5014  
ISSN: 0019-9567

Language: ENGLISH Document Type: ARTICLE

Abstract: The majority of in vitro-grown *Neisseria gonorrhoeae* strains were unable to use hemoglobin as the sole source of iron for growth (Hgb(-)), but a minor population was able to do so (Hgb(+)). The ability of Hgb(+) gonococci to utilize hemoglobin as the iron source was associated with the expression of an iron-repressible 89-kDa hemoglobin-binding protein in the outer membrane. The N-terminal amino acid sequence of this protein revealed amino acids, from positions 2 to 16, identical to those of HpuB, an 85 kDa iron-regulated hemoglobin-haptoglobin utilization outer membrane protein of *Neisseria meningitidis*. Isogenic mutants constructed by allelic replacement with a meningococcal hpu::mini-Tn3erm construct no longer expressed the 89-kDa protein. Mutants could not utilize hemoglobin to support growth but still grew on heme. Thus, the gonococcal HpuB homolog is a functional hemoglobin receptor and is essential for growth with hemoglobin.

3/3,AB/9 (Item 2 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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05165015 Genuine Article#: VE443 Number of References: 41

Title: OUTER-MEMBRANE PROTEIN B1, AN IRON-REPRESSIBLE PROTEIN CONSERVED IN THE OUTER-MEMBRANE OF MORAXELLA (BRANHAMELLA) CATARRHALIS, BINDS HUMAN TRANSFERRIN (Abstract Available)

Author(s): CAMPAGNARI AA; DUCEY TF; REBMANN CA

Corporate Source: SUNY BUFFALO,DIV INFECT DIS,DEPT MED,BIOMED RESBLDG,3435 BAILEY AVE/BUFFALO//NY/14214; SUNY BUFFALO,DEPT MICROBIOL/BUFFALO//NY/14214; SUNY BUFFALO,DEPT CLIN LAB SCI/BUFFALO//NY/14214

Journal: INFECTION AND IMMUNITY, 1996, V64, N9 (SEP), P3920-3924

ISSN: 0019-9567

Language: ENGLISH Document Type: ARTICLE

Abstract: *Moraxella* (*Branhamella*) *catarrhalis* is a gram-negative human mucosal pathogen, which primarily causes otitis media in young children. However, this bacterium is also a common cause of lower respiratory tract infections in adults with underlying lung disease. Our previous data have shown that *M. catarrhalis* expresses iron-repressible outer membrane proteins in response to iron limitation. We have extended these observations to demonstrate that one of these proteins, termed outer membrane protein (OMP) B1, binds human transferrin. Using a newly developed monoclonal antibody to OMP B1, we determined that this protein is conserved in the iron-stressed outer membranes of all clinical isolates of *M. catarrhalis* tested to date. Furthermore, our data have confirmed that children infected with *M. catarrhalis* have immunoglobulin G antibodies to OMP B1 in their convalescent sera. These current data suggest that OMP B1 is immunogenic and expressed in vivo and may be involved in an iron uptake mechanism utilized by *M. catarrhalis*.

3/3,AB/10 (Item 3 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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05021840 Genuine Article#: UZ996 Number of References: 54

Title: UTILIZATION OF HEMIN AND HEMOGLOBIN BY VIBRIO-VULNIFICUS BIOTYPE-2 (Abstract Available)

Author(s): FOUZ B; MAZOY R; LEMOS ML; DELOLMO MJ; AMARO C

Corporate Source: UNIV VALENCIA,DEPT MICROBIOL,FAC BIOL,AVDA DR MOLINER 50/E-46100 BURJASSOT/VALENCIA/SPAIN/; UNIV VALENCIA,DEPT MICROBIOL,FAC BIOL/E-46100 BURJASSOT/VALENCIA/SPAIN/; UNIV SANTIAGO DE COMPOSTELA,DEPT MICROBIOL & PARASITOL,FAC CIENCIAS/E-27002 LUGO//SPAIN/

Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1996, V62, N8 (AUG), P 2806-2810

ISSN: 0099-2240

Language: ENGLISH Document Type: ARTICLE

Abstract: The eel pathogen *Vibrio vulnificus* biotype 2 is able to use

hemoglobin (Hb) and heme (Hm) to reverse iron limitation. In this study, the adjuvant effect of both compounds on eel pathogenicity has been evaluated and confirmed. Further, we have studied the heme-iron acquisition mechanism displayed by this bacterium. Whole cells were capable of binding Hb and Hm, independently of (i) iron levels in growth medium and (ii) the presence of polysaccharide capsules on bacterial surface. The Hb- and Hm-binding capacity was retained by the outer membrane protein (OMP) fraction and was abolished after proteolytic digestion of OMP samples. Western blotting (immunoblotting) of denatured OMPs revealed that two major protein bands of 36 and 32 kDa were involved in both Km and Hb binding. The expression of these proteins was not affected by iron levels. In addition, *V. vulnificus* biotype 2 produced extracellular proteases, not regulated by iron, that were active against native Hb. In conclusion, the overall data suggest that the eel pathogen *V. vulnificus* biotype 2 can obtain iron by means of a mechanism which involves a direct interaction between the heme moiety and constitutive OMPs.

3/3,AB/11 (Item 4 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2004 Inst for Sci Info. All rts. reserv.

05011765 Genuine Article#: UZ047 Number of References: 51  
Title: HMBR OUTER-MEMBRANE RECEPTORS OF PATHOGENIC NEISSERIA SPP -  
IRON-REGULATED, HEMOGLOBIN-BINDING PROTEINS WITH A HIGH-LEVEL OF  
PRIMARY STRUCTURE CONSERVATION (Abstract Available)  
Author(s): STOJILJKOVIC I; LARSON J; HWA V; ANIC S; SO M  
Corporate Source: OREGON HLTH SCI UNIV, DEPT MOLEC MICROBIOL &  
IMMUNOL/PORTLAND//OR/97201; EMORY UNIV, DEPT MICROBIOL &  
IMMUNOL/ATLANTA//GA/30322  
Journal: JOURNAL OF BACTERIOLOGY, 1996, V178, N15 (AUG), P4670-4678  
ISSN: 0021-9193  
Language: ENGLISH Document Type: ARTICLE  
Abstract: We have recently cloned and characterized the hemoglobin receptor gene from *Neisseria meningitidis* serogroup C. *N. meningitidis* cells expressing HmbR protein were able to bind biotinylated hemoglobin, and the binding was specifically inhibited by unlabeled hemoglobin and not heme. The HmbR-mediated hemoglobin binding activity of *N. meningitidis* cells was shown to be iron regulated. The presence of hemoglobin but not heme in the growth medium stimulated HmbR-mediated hemoglobin binding activity. The efficiency of utilization of different hemoglobins by the HmbR-expressing *N. meningitidis* cells was shown to be species specific; human hemoglobin was the best source of iron, followed by horse, rat, turkey, dog, mouse, and sheep hemoglobins. The phenotypic characterization of HmbR mutants of some clinical strains of *N. meningitidis* suggested the existence of two unrelated hemoglobin receptors. The HmbR-unrelated hemoglobin receptor was shown to be identical to Hpu, the hemoglobin-haptoglobin receptor of *N. meningitidis*. The Hpu-dependent hemoglobin utilization system was not able to distinguish between different sources of hemoglobin; all animal hemoglobins were utilized equally well. HmbR-like genes are also present in *N. meningitidis* serogroups A and B, *Neisseria gonorrhoeae* MS11 and FA19, *Neisseria perflava*, and *Neisseria polysaccharea*. The hemoglobin receptor genes from *N. meningitidis* serogroups A and B and *N. gonorrhoeae* MS11 were cloned, and their nucleotide sequences were determined. The nucleotide sequence identity ranged between 86.5% (for *N. meningitidis* serogroup B hmbR and MS11 hmbR) and 93.4% (for *N. meningitidis* serogroup B hmbR and *N. meningitidis* serogroup C hmbR). The deduced amino acid sequences of these neisserial hemoglobin receptors were also highly related, with overall 84.7% conserved amino acid residues. A stop codon was found in the hmbR gene of *N. gonorrhoeae* MS11. This strain was still able to use hemoglobin and hemoglobin-haptoglobin complexes as iron sources, indicating that some gonococci may express only the HmbR-independent hemoglobin utilization system.

3/3,AB/12 (Item 5 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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04980181 Genuine Article#: UW876 Number of References: 14  
Title: ONE-STEP METAL-AFFINITY METHOD FOR THE PURIFICATION OF THE  
IRON-BINDING PROTEIN FBP OF %NEISSERIA%-MENINGITIDIS% (Abstract  
Available)  
Author(s): FERRON L; PINTOR M; GOMEZ JA; CRIADO MT; FERREIROS C  
Corporate Source: UNIV SANTIAGO DE COMPOSTELA,FAC FARM,DEPT MICROBIOL &  
PARASITOL/SANTIAGO COMPOSTE//SPAIN/; UNIV SANTIAGO DE COMPOSTELA,FAC  
FARM,DEPT MICROBIOL & PARASITOL/SANTIAGO COMPOSTE//SPAIN/  
Journal: JOURNAL OF MICROBIOLOGICAL METHODS, 1996, V25, N3 (JUN), P233-236  
ISSN: 0167-7012  
Language: ENGLISH Document Type: ARTICLE  
Abstract: A one-step method for the purification of the iron-binding  
protein, Fbp, from %Neisseria% meningitidis% has been developed using  
affinity chromatography on iron-Sepharose. This method allowed the  
purification of the protein in non-denaturing conditions and in a  
similar way to those used previously. Our results demonstrate the  
homogeneity of the purified protein as tested by SDS-PAGE and IEF.

3/3,AB/13 (Item 6 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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04839868 Genuine Article#: UL527 Number of References: 68  
Title: ACQUISITION OF IRON BY THE NON-SIDEROPHORE-PRODUCING  
PSEUDOMONAS-FRAGI (Abstract Available)  
Author(s): CHAMPOMIERVERGES MC; STINTZI A; MEYER JM  
Corporate Source: UNIV STRASBOURG 1,CNRS,URA D1481,LAB MICROBIOL & GENET,28  
RUE GOETHE/F-67083 STRASBOURG//FRANCE/; UNIV STRASBOURG 1,CNRS,URA  
D1481,LAB MICROBIOL & GENET/F-67083 STRASBOURG//FRANCE/; INRA,LAB RECH  
VIANDE/F-78352 JOUY EN JOSAS//FRANCE/  
Journal: MICROBIOLOGY-UK, 1996, V142, MAY (MAY), P1191-1199  
ISSN: 1350-0872  
Language: ENGLISH Document Type: ARTICLE  
Abstract: The iron requirement, siderophore production and iron uptake  
mechanism of the type strain Pseudomonas fragi ATCC 4973 and five P.  
fragi isolates from meat were analysed. The strains exhibited a high  
sensitivity to iron starvation: their growth was strongly inhibited in  
medium supplemented with the iron chelator ethylenediamine  
di(hydroxyphenylacetic acid) or in medium treated with  
8-hydroxyguinoline to remove contaminating iron. No siderophores were  
detectable in the growth supernatants of iron-starved cells.  
Cross-feeding experiments in iron-depleted medium showed, however, that  
the bacterial growth could be strongly stimulated by siderophores of  
foreign origin including desferriferrioxamine B, enterobactin and some  
pyoverdines. Moreover, all the strains were capable of efficiently  
using the iron sources present in their natural environment, i.e.  
transferrin, lactoferrin and haemoglobin. Iron starvation led to the  
specific production of supplementary outer-membrane proteins of  
apparent molecular mass ranging from 80 to 88 kDa. Furthermore, growth  
in the presence of exogenous siderophores resulted, in some strains, in  
the induction of siderophore-mediated iron uptake systems. For one  
strain the concomitant synthesis of an iron-regulated,  
siderophore-inducible outer-membrane protein was observed.

3/3,AB/14 (Item 7 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2004 Inst for Sci Info. All rts. reserv.

04635265 Genuine Article#: TY365 Number of References: 48  
Title: SIDEROPHORE-MEDIATED IRON ACQUISITION MECHANISMS IN  
VIBRIO-VULNIFICUS BIOTYPE-2 (Abstract Available)  
Author(s): BIOSCA EG; FOUZ B; ALCAIDE E; AMARO C  
Corporate Source: UNIV VALENCIA,FAC BIOL,DEPT MICROBIOL & ECOL,AVDA DR  
MOLINER 50/E-46100 VALENCIA//SPAIN/; UNIV VALENCIA,FAC BIOL,DEPT



MICROBIOL & ECOL/E-46100 VALENCIA//SPAIN/  
Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1996, V62, N3 (MAR), P  
928-935

ISSN: 0099-2240

Language: ENGLISH Document Type: ARTICLE

Abstract: *Vibrio vulnificus* biotype 2 is a primary pathogen for eels and, as has recently been suggested, an opportunistic pathogen for humans. In this study we have investigated the ability of *V. vulnificus* biotype 2 to obtain iron by siderophore-mediated mechanisms and evaluated the importance of free iron in vibriosis. The virulence degree for eels was dependent on iron availability from host fluids, as was revealed by a reduction in the 50% lethal dose for iron-overloaded eels. This biotype produced both phenolate- and hydroxamate-type siderophores of an unknown nature and two new outer membrane proteins of around 84 and 72 kDa in response to iron starvation. No alterations in lipopolysaccharide patterns were detected in response to iron stress. Finally, our data suggest that *V. vulnificus* biotype 2 uses the hydroxamate-type siderophore for removal of iron from transferrin rather than relying on a receptor for this iron-binding protein.

3/3,AB/15 (Item 8 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2004 Inst for Sci Info. All rts. reserv.

01920368 Genuine Article#: JL957 Number of References: 60  
Title: FUR REGULATION IN *YERSINIA SPECIES* (Abstract Available)  
Author(s): STAGGS TM; PERRY RD  
Corporate Source: UNIV KENTUCKY,DEPT MICROBIOL & IMMUNOL,MS415 CHANDLER MED  
CTR/LEXINGTON//KY/40536; UNIV KENTUCKY,DEPT MICROBIOL & IMMUNOL,MS415  
CHANDLER MED CTR/LEXINGTON//KY/40536  
Journal: MOLECULAR MICROBIOLOGY, 1992, V6, N17 (SEP), P2507-2516  
ISSN: 0950-382X

Language: ENGLISH Document Type: ARTICLE

Abstract: The effects of iron have been linked with several phenomena including regulation of membrane proteins; however, the mechanism of iron regulation is not well characterized in *Yersinia pestis*. It is well known that in *Escherichia coli*, the *%fur%* *%gene%* product mediates negative transcriptional regulation of several genes in response to iron. We have cloned a *Y. pestis* *%fur%* *%gene%* which is highly homologous to the *E. coli* *%fur%* regulatory *%gene%*. The sequence of the *Y. pestis* *%fur%* *%gene%* exhibits 75% homology to the *E. coli* gene at the nucleotide level, and 84% homology at the predicted amino acid level. The *Y. pestis* *%fur%* *%gene%* is transcribed as a single gene message of approximately 0.5 kb which encodes an approximately 16 kDa protein when expressed in *E. coli* minicells. A *Yersinia enterocolitica* *fur* mutant exhibits hypersensitivity to the *Y. pestis* bacteriocin, pesticin; the cloned *Y. pestis* *%fur%* *%gene%* restores wild-type levels of pesticin sensitivity. Furthermore, iron regulation of at least five surface proteins in this *Y. enterocolitica* *fur* mutant is restored by transcomplementation with the *Y. pestis* *%fur%* *%gene%*. These data indicate that *Y. pestis* and *Y. enterocolitica* possess homologous *Fur* systems which regulate expression of proteins in response to iron availability.

3/3,AB/16 (Item 9 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2004 Inst for Sci Info. All rts. reserv.

01740384 Genuine Article#: HX278 Number of References: 46  
Title: CLONING, SEQUENCING, AND TRANSCRIPTIONAL REGULATION OF VIUA, THE GENE ENCODING THE FERRIC VIBRIOBACTIN RECEPTOR OF *VIBRIO-CHOLERA*E (Abstract Available)  
Author(s): BUTTERTON JR; STOEBNER JA; PAYNE SM; CALDERWOOD SB  
Corporate Source: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114;  
MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114; UNIV  
TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712; HARVARD UNIV,SCH MED,DEPT  
MICROBIOL & GENET/BOSTON//MA/02115

Journal: JOURNAL OF BACTERIOLOGY, 1992; V174, N11 (JUN), P3729-3738

Language: ENGLISH Document Type: ARTICLE

Abstract: A 74-kDa iron-regulated outer membrane protein of *Vibrio cholerae* acts as the receptor for the *V. cholerae* iron-siderophore complex, ferric vibriobactin. MBG14, a mutant of *V. cholerae* 0395 containing a *TnphoA* insertion in a gene designated *viuA*, lacks this 74-kDa outer membrane protein and is unable to bind or utilize exogenous ferric vibriobactin. Introduction of a plasmid containing the complete *viuA* coding sequence and 513 bp of upstream DNA into MBG14 restored ferric vibriobactin utilization to the mutant. The DNA insert in this plasmid was sequenced, revealing a single open reading frame of 2,061 bp, encoding a deduced protein of 687 amino acids with a predicted molecular mass of 76,417 Da and a predicted initial signal sequence of 37 amino acids. *ViuA* showed only weak homology to two iron-regulated outer membrane proteins in *Escherichia coli*, *IutA* and *FecA*. Construction of *viuA::TnphoA* gene fusions allowed study of the regulation of *viuA* expression by iron. This regulation in *E. coli* was dependent on the *%fur%* *%gene%*. Northern (RNA) blot analysis of RNA from wild-type *V. cholerae* grown in high- and low-iron media revealed a monocistronic *viuA* message that was negatively regulated by iron at the transcriptional level. Primer extension analysis identified a single transcriptional start site, located 243 bp above the translational start site. The promoter region of *viuA* contained two interrupted dyad symmetric nucleotide sequences, overlapping the -10 and -35 boxes, each similar to the *E. coli* *Fur* binding consensus sequence. Another iron-regulated gene in *V. cholerae* that is negatively regulated by *fur*, *irgA*, requires a positive transcriptional activator (*irgB*) for expression. However, a strain of *V. cholerae* mutant in *irgB* was unaffected in *viuA* expression. These studies suggest that there is conserved, global coordinate iron regulation in *V. cholerae* by *fur*; additional regulatory factors, superimposed upon the *fur* system, may provide more precise control of individual iron-regulated genes.

3/3,AB/17 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2004 American Chemical Society. All rts. reserv.

139241254 CA: 139(16)241254e JOURNAL

Identification of iron-activated and -repressed *Fur*-dependent genes by transcriptome analysis of *Neisseria meningitidis* group B

AUTHOR(S): Grifantini, Renata; Sebastian, Shite; Frigimelica, Elisabetta; Draghi, Monia; Bartolini, Erika; Muzzi, Alessandro; Rappuoli, Rino; Grandi, Guido; Genco, Caroline Attardo

LOCATION: Chiron SpA, Siena, Italy

JOURNAL: Proc. Natl. Acad. Sci. U. S. A. (Proceedings of the National Academy of Sciences of the United States of America) DATE: 2003 VOLUME:

100 NUMBER: 16 PAGES: 9542-9547 CODEN: PNASA6 ISSN: 0027-8424

LANGUAGE: English PUBLISHER: National Academy of Sciences

3/3,AB/18 (Item 2 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2004 American Chemical Society. All rts. reserv.

130071518 CA: 130(6)71518p PATENT

Live attenuated bacterial vaccines containing a modified iron uptake *fur* gene

INVENTOR(AUTHOR): Baldwin, Thomas John; Borriello, Saverio Peter; Palmer, Helen Mary

LOCATION: UK,

ASSIGNEE: Medical Research Council

PATENT: PCT International ; WO 9856901 A2 DATE: 19981217

APPLICATION: WO 98GB1683 (19980609) \*GB 9711964 (19970609)

PAGES: 49 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A

DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; GW; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU;

applicor

ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS  
; MW; SD; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT;  
LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG

3/3,AB/19 (Item 1 from file: 654)  
DIALOG(R)File 654:US Pat.Full.  
(c) Format only 2004 The Dialog Corp. All rts. reserv.

0005335587  
Derwent Accession: 2003-787326  
Compositions and methods for treatment of neoplastic disease  
Inventor: David Terman, INV  
Correspondence Address: David S. Terman, P.O. Box 987, Pebble beach, CA,  
93953, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20030157113	A1	20030821	US 2000751708	20001228
Provisional				US 60-173371	19991228

Fulltext Word Count: 151651

Abstract:

The present invention comprises compositions and methods for treating a tumor or neoplastic disease in a host, The methods employ conjugates comprising superantigen polypeptides, nucleic acids with other structures that preferentially bind to tumor cells and are capable of inducing apoptosis. Also provided are superantigen-glycolipid conjugates and vesicles that are loaded onto antigen presenting cells to activate both T cells and NKT cells. Cell-based vaccines comprise tumor cells engineered to express a superantigen along with glycolipids products which, when expressed, render the cells capable of eliciting an effective anti-tumor immune response in a mammal into which these cells are introduced. Included among these compositions are tumor cells, hybrid cells of tumor cells and accessory cells, preferably dendritic cells. Also provided are tumoricidal T cells and NKT cells devoid of inhibitory receptors or inhibitory signaling motifs which are hyperresponsive to the the above compositions and lipid-based tumor associated antigens that can be administered for adoptive immunotherapy of cancer and infectious diseases.

3/3,AB/20 (Item 2 from file: 654)  
DIALOG(R)File 654:US Pat.Full.  
(c) Format only 2004 The Dialog Corp. All rts. reserv.

0005329374  
Derwent Accession: 2003-897737  
Staphylococcus aureus genes and polypeptides  
Inventor: Andrew Simpson, INV  
Gil Choi, INV  
Assignee: Human Genome Sciences, Inc. (03), Rockville, MD, 20850, US, 9410  
Key West Avenue  
Correspondence Address: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE,  
ROCKVILLE, MD, 20850

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20030153733	A1	20030814	US 2002278946	20021024
Division	US 6521441			US 2002830217	20020115
A371	PENDING			WO 99US6199	19990318
Provisional				US 60-78862	19980320
Provisional				US 60-80296	19980401

7

A Applicant

Fulltext Word Count: 34439

## Abstract:

The present invention relates to 11 novel genes from *S. aureus* and the polypeptides they encode. Also provided as are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of *S. aureus* polypeptide activity. The invention additionally relates to diagnostic methods for detecting *Staphylococcus* nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by *Staphylococcus*.

3/3,AB/21 (Item 3 from file: 654)

DIALOG(R)File 654:US Pat.Full.

(c) Format only 2004 The Dialog Corp. All rts. reserv.

0005126116

Derwent Accession: 2003-361759

Compositions and methods for treatment of neoplastic disease

Inventor: David Terman, INV

Correspondence Address: David S. Terman, P.O. Box 987, Pebble Beach, CA, 93953, US

	Publication Number	Kind	Date	Application Number	Filing Date
	-----	--	-----	-----	-----
Main Patent	US 20020177551	A1	20021128	US 2001870759	20010530
Provisional				US 60-208128	20000531

Fulltext Word Count: 164990

## Abstract:

The present invention comprises compositions and methods for treating a tumor or neoplastic disease in a host, The methods employ conjugates comprising superantigen polypeptides, nucleic acids with other structures that preferentially bind to tumor cells and are capable of inducing apoptosis. Also provided are superantigen-glycolipid conjugates and vesicles that are loaded onto antigen presenting cells to activate both T cells and NKT cells. Cell-based vaccines comprise tumor cells engineered to express a superantigen along with glycolipids products which, when expressed, render the cells capable of eliciting an effective anti-tumor immune response in a mammal into which these cells are introduced. Included among these compositions are tumor cells, hybrid cells of tumor cells and accessory cells, preferably dendritic cells. Also provided are tumoricidal T cells and NKT cells devoid of inhibitory receptors or inhibitory signaling motifs which are hyperresponsive to the the above compositions and lipid-based tumor associated antigens that can be administered for adoptive immunotherapy of cancer and infectious diseases.

3/3,AB/22 (Item 4 from file: 654)

DIALOG(R)File 654:US Pat.Full.

(c) Format only 2004 The Dialog Corp. All rts. reserv.

0004920283

Derwent Accession: 2001-398123

Antigen preparations

Inventor: Thomas Baldwin, INV

Paul Williams, INV

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Correspondence Address: KLARQUIST SPARKMAN CAMPBELL LEIGH & WHINSTON,  
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, OR, 97204-2988, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20010031268	A1	20011018	US 2000740048	20001218
Provisional				US 60-172485	19991217

Fulltext Word Count: 7244

Abstract:

Bacterial antigen preparations for use as live or killed immunogens and vaccines can be produced by culture of bacteria such as Neisseria in medium comprising norepinephrine or other catechol-group-containing growth inducer of bacterial growth, harvesting and pharmaceutical formulation. The antigen preparations can comprise bacterial protein(s) inducible by norepinephrine.

3/3,AB/23 (Item 5 from file: 654)  
DIALOG(R)File 654:US Pat.Full.  
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4826849

Derwent Accession: 1999-580304

Utility

C/ Staphylococcus aureus genes and polypeptides

Inventor: Simpson, Andrew J. G., Sao Paulo, BR

Choi, Gil H., Rockville, MD

Assignee: Human Genome Sciences, Inc. (02), Rockville, MD

Ludwig Institute For Cancer Research (03), Sao Paulo, BR

Human Genome Sciences Inc

Ludwig Institite for Cancer Research BR

Ludwig Inst For Cancer Res BR (Code: 38350 64358)

Examiner: Navarro, Mark (Art Unit: 165)

Law Firm: Human Genome Sciences, Inc.

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 6521441	A	20030218	US 2002830217	20020115
PCT	WO 9947662		19990923	WO 99US6199	19990318

371:  
102e:

Fulltext Word Count: 32270

Abstract:

The present invention relates to 11 novel genes from S. aureus and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity. The invention additionally relates to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by Staphylococcus.

3/3,AB/24 (Item 6 from file: 654)  
DIALOG(R)File 654:US Pat.Full.

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4180640

Derwent Accession: 1999-468143

Utility

CERTIFICATE OF CORRECTION

C/ Method and materials for detecting Legionella pneumophila

Inventor: Cianciotto, Nicholas P., Evanston, IL

Hickey, Erin K., Evanston, IL

Assignee: Northwestern University (02), Evanston, IL

Northwestern University (Code: 60920)

Examiner: Myers, Carla J. (Art Unit: 164)

Law Firm: Sheridan Ross P.C.

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5935782	A	19990810	US 96766858	19961213
Provisional				US 60-11545	19960213

Fulltext Word Count: 15861

Abstract:

The invention provides novel genes and proteins of Legionella pneumophila. The invention also provides methods of detecting or quantitating L. pneumophila using these genes, mRNAs encoded by the genes, or proteins encoded by the genes as targets. Nucleic acids designed to hybridize with the genes or mRNAs encoded by the genes, or antibodies that bind specifically to the proteins, are used in the methods, and the nucleic acids and antibodies can be provided in kits.

3/3,AB/25 (Item 1 from file: 71)

DIALOG(R)File 71:ELSEVIER BIOBASE

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00040756 94088062

Cloning and sequence analysis of the %fur% %gene% encoding an iron-regulatory protein of %Neisseria% %meningitidis%

Karhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.

ADDRESS: R.R. Karhoff-Schweizer, Canada

Journal: Gene, 141/1 (139-140), 1994

PUBLICATION DATE: 19940000

CODEN: GENED

ISSN: 0378-1119

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

3/3,AB/26 (Item 1 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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01021406

HUMAN GENES AND GENE EXPRESSION PRODUCTS ISOLATED FROM HUMAN PROSTATE  
GENES HUMAINS ET PRODUITS D'EXPRESSION GENIQUES ISOLEES D'UNE PROSTATE  
HUMAINE

Patent Applicant/Assignee:

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STACHE-CRAIN Birgit, 345 South Mary Avenue, Sunnyvale, CA 94086, US, US  
(Residence), DE (Nationality), (Designated only for: US)  
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, US (Nationality), (Designated only for: US)

Legal Representative:

BLACKBURN Robert P (agent), Chiron Corporation, P.O. Box 8097,  
Emeryville, CA 94662-8097 (et al), US,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200350236 A2 20030619 (WO 0350236)  
Application: WO 2002US28214 20020904 (PCT/WO US0228214)  
Priority Application: US 200112697 20011207

Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU  
CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP  
KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO  
RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW  
(EP) AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LU MC NL PT SE SK TR  
(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG  
(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW  
(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English

Fulltext Word Count: 86998

English Abstract

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-1477. The polypeptides of the invention correspond to a polypeptide comprising the amino acid sequence information of at least one of SEQ ID NOS:1478-1568.

French Abstract

L'invention se rapporte a de nouveaux polynucleotides humains et a leurs variantes, a leurs polypeptides codes et a leurs variantes, aux genes correspondant a ces polynucleotides et aux proteines exprimees par les genes. L'invention se rapporte egalement a des diagnostics et des therapies comprenant lesdits nouveaux polynucleotides humains, leurs genes correspondants ou leurs produits genetiques, y compris les sondes, les nucleotides antisens et les anticorps. Les polynucleotides de cette invention correspondent a un polynucleotide comprenant l'information de sequence d'au moins une des SEQ ID NOS:1-1477. Les polypeptides de cette invention correspondent, quant a eux, a un polypeptide comprenant l'information d'une sequence d'acides amines d'au moins une des SEQ ID

NOS:1478-1568.

3/3,AB/27 (Item 2 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT  
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00922886

HUMAN GENES AND GENE EXPRESSION PRODUCTS ISOLATED FROM HUMAN PROSTATE  
GENES HUMAINS ET PRODUITS D'EXPRESSION GENETIQUE ISOLEES DE LA PROSTATE  
HUMAINE

Patent Applicant/Assignee:

CHIRON CORPORATION, 4560 Horton Street, R440, Emeryville, CA 94608, US,  
US (Residence), US (Nationality), (For all designated states except:  
US)

HYSEQ INC, 675 Almanor Avenue, Sunnyvale, CA 94086, US, US (Residence),  
US (Nationality), (For all designated states except: US)

Patent Applicant/Inventor:

ESCOBEDO Jaime, 1470 Lavorna Road, Alamo, CA 94507, US, US (Residence),  
CL (Nationality), (Designated only for: US)

GARCIA Pablo Dominguez, 882 Chenery Street, San Francisco, CA 94131, US,  
US (Residence), CL (Nationality), (Designated only for: US)

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LAMSON George, 232 Sandringham Drive, Moraga, CA 94556, US, US  
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Patent and Priority Information (Country, Number, Date):

Patent: WO 200255700 A2-A3 20020718 (WO 0255700)

Application: WO 2001US47349 20011207 (PCT/WO US0147349)

Priority Application: US 2000254648 20001207; US 2001275688 20010313

Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU

CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP

KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO

RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG

(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW

(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English

Fulltext Word Count: 87496

English Abstract

This invention relates to novel human polynucleotides and variants



thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-1477. The polypeptides of the invention correspond to a polypeptide comprising the amino acid sequence information of at least one of SEQ ID NOS:1478-1568.

#### French Abstract

L'invention concerne de nouveaux polynucleotides humains et des variants de ceux-ci, leurs polypeptides codes et les variants de ceux-ci, des genes correspondant a ces polynucleotides et des proteines exprimees par ces genes. L'invention concerne egalement des diagnostics et therapies utilisant ces nouveaux polynucleotides humains, leurs genes correspondants ou leurs produits genetiques, y compris des sondes, des nucleotides antisens et des anticorps. Les polynucleotides decrits par la presente invention correspondent a un polynucleotide contenant les informations de sequence d'au moins un des SEQ ID NOS:1-1477. Les polypeptides decrits par la presente invention correspondent a un polypeptide comprenant des informations de sequence aminoacide d'au moins une des sequences SEQ ID NOS:1478-1568.

3/3,AB/28 (Item 3 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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00812075

#### ANTIGEN PREPARATIONS

#### PREPARATIONS D'ANTIGENES

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#### Patent and Priority Information (Country, Number, Date):

Patent: WO 200144278 A2-A3 20010621 (WO 0144278)

Application: WO 2000GB4874 20001218 (PCT/WO GB0004874)

Priority Application: GB 9929923 19991217

Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ

DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ

LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG

SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

(OA) BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG

(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZW

(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English  
Fulltext Word Count: 6587

English Abstract

Bacterial antigen preparations for use as live or killed immunogens and vaccines can be produced by culture of bacteria such as Neisseria in medium comprising norepinephrine or other catechol-group-containing growth inducer of bacterial growth, harvesting and pharmaceutical formulation. The antigen preparations can comprise bacterial protein(s) inducible by norepinephrine.

French Abstract

Cette invention se rapporte a des preparations d'antigenes bacteriens destines a servir d'immunogenes et de vaccins vivants ou tues, qui peuvent etre produites par culture de bacteries telles que Neisseria, dans un milieu comprenant de la norepinephrine ou tout autre inducteur de croissance bacterienne contenant un groupe catechol, par recolte et par formulation pharmaceutique. Ces preparations d'antigene peuvent contenir une/des proteine(s) bacterienne(s) induisible(s) par la norepinephrine.

3/3,AB/29 (Item 4 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT  
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00749502

NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS  
GENES BACTERIENS ESSENTIELS ET LEURS PROTEINES  
NEUE ESSENTIELLE BAKTERIELLE GENE UND IHRE PROTEINE

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Patent and Priority Information (Country, Number, Date):

Patent: WO 200061792 A1 20001019 (WO 0061792)  
Application: WO 2000EP2713 20000328 (PCT/WO EP0002713)  
Priority Application: DE 19916176 19990410

Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE

DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC  
LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK  
SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

(OA) BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG

(AP) GH GM KE LS MW SD SL SZ TZ UG ZW

(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: German

Filing Language: German

Fulltext Word Count: 14072

English Abstract

The invention relates to nucleic acids and to protein sequences derived from said nucleic acids which possess functions that are essential to the survival of Escherichia coli. The invention also relates to vectors and host cells that have been transformed with these vectors for expressing essential proteins of the type described above and to proteins produced

with these vectors. Finally, the invention also relates to the use of the proteins produced with these vectors in screening methods for identifying antibacterial substances and to the antibacterial substances found with these proteins.

#### French Abstract

L'invention concerne des acides nucleiques et leurs sequences proteiques derivees, qui possedent des fonctions essentielles a la vie d'Escherichia coli; des vecteurs et des cellules hotes, transformees au moyen desdits vecteurs, qui permettent l'expression desdites proteines essentielles et les proteines produites au moyen desdits vecteurs; ainsi que l'utilisation des proteines produites au moyen desdits vecteurs dans des techniques de criblage qui permettent de rechercher des substances antibacteriennes et les substances antibacteriennes trouvees au moyen desdites proteines.

#### German Abstract

Die Erfindung betrifft Nucleinsauren und davon abgeleitete Proteinsequenzen, die fur das Überleben von Escherichia coli essentielle Funktionen besitzen. Sie umfasst daruber hinaus Vektoren und mit diesen transformierte Wirtszellen zur Expression solcher essentiellen Proteine sowie die mit diesen Vektoren erzeugten Proteine. Sie umfasst weiter die Verwendung der mit diesen Vektoren erzeugten Proteine in Screeningverfahren zur Auffindung antibakterieller Substanzen sowie der mit diesen Proteinen gefundenen antibakteriellen Substanzen.

3/3,AB/30 (Item 5 from file: 349)

DIALOG(R) File 349:PCT FULLTEXT

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00516310

i(STAPHYLOCOCCUS AUREUS) GENES AND POLYPEPTIDES

GENES ET POLYPEPTIDES DU STAPHYLOCOQUE DORE

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Patent and Priority Information (Country, Number, Date):

Patent: WO 9947662 A1 19990923

Application: WO 99US6199 19990318 (PCT/WO US9906199)

Priority Application: US 9878682 19980320; US 9880296 19980401; US  
9884674 19980507

Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES

FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV  
MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG  
US UZ VN YU ZW GH GM KE LS MW SD SL SZ UG ZW AM AZ BY KG KZ MD RU TJ TM  
AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM  
GA GN GW ML MR NE SN TD TG

Publication Language: English

Fulltext Word Count: 32916

#### English Abstract

The present invention relates to 11 novel genes from i(S. aureus) and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of i(S. aureus) polypeptide activity. The invention additionally relates to diagnostic methods for detecting i(Staphylococcus) nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by i(Staphylococcus).

#### French Abstract

La presente invention concerne 11 genes issus du staphylocoque dore et les polypeptides qu'ils codent. L'invention concerne egalement des vecteurs, ces cellules hotes, des anticorps et des procedes a recombinaison permettant de les obtenir. L'invention concerne aussi des techniques de recherche systematique permettant d'identifier des agonistes et des antagonistes de l'activite polypeptide du staphylocoque dore. L'invention concerne en outre des techniques de diagnostic permettant de detecter dans un echantillon biologique des acides nucleiques, des polypeptides et des anticorps du staphylocoque dore. L'invention concerne enfin des vaccins permettant la prevention ou l'attenuation de l'infection par le staphylocoque.

3/3,AB/31 (Item 6 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT  
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00516287

i(STAPHYLOCOCCUS) AUREUS GENES AND POLYPEPTIDES  
GENES ET POLYPEPTIDES DU i(STAPHYLOCOCCUS AUREUS)

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Patent and Priority Information (Country, Number, Date):

Patent: WO 9947639 A2 19990923  
Application: WO 99US5976 19990319 (PCT/WO US9905976)  
Priority Application: US 9878682 19980320; US 9880296 19980401; US  
9884674 19980507

Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES  
FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV  
MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG  
US UZ VN YU ZW GH GM KE LS MW SD SL SZ UG ZW AM AZ BY KG KZ MD RU TJ TM  
AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM  
GA GN GW ML MR NE SN TD TG

Publication Language: English

Fulltext Word Count: 34491

English Abstract

The present invention relates to 11 novel genes from i(S. aureus) and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of i(S. aureus) polypeptide activity. The invention additionally relates to diagnostic methods for detecting i(Staphylococcus) nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by i(Staphylococcus).

French Abstract

L'invention porte sur 11 nouveaux genes du i(Staphylococcus aureus), sur les polypeptides pour lesquels ils codent, et sur des vecteurs, des cellules hotes, des anticorps et des methodes de recombinaison pour les produire. L'invention porte en outre sur des methodes de criblage permettant d'identifier l'activite d'agonistes et d'antagonistes des polypeptides du i(Staphylococcus aureus), sur des procedes diagnostiques de detection des acides nucleiques, des polypeptides et des anticorps du i(Staphylococcus aureus) dans un echantillon biologique, et sur de nouveaux vaccins prevenant ou attenuant les infections par le i(Staphylococcus).

3/3,AB/32 (Item 7 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT

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00466436

LIVE ATTENUATED VACCINES

VACCIN VIVANT ATTENUÉ

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Patent and Priority Information (Country, Number, Date):

Patent: WO 9856901 A2 19981217

Application: WO 98GB1683 19980609 (PCT/WO GB9801683)

Priority Application: GB 9711964 19970609

Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES

FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD

MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US

UZ VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE

CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN

ML MR NE SN TD TG

Publication Language: English

Fulltext Word Count: 12457

English Abstract

An attenuated bacterium in which the native i(%fur%) %gene%, or homologue thereof, is modified such that the expression of the i(%fur%) %gene% product, or homologue thereof, is regulated independently of the iron concentration in the environment of the bacterium, is suitable for use as a live vaccine. The bacterium may be, in particular, i(%Neisseria% %meningitidis%).

French Abstract

On décrit une bactérie atténuée dans laquelle le gène i(fur) natif ou son homologue est modifié de sorte que l'expression du produit génique i(fur) ou son homologue est régulée indépendamment de la concentration en fer dans l'environnement de la bactérie. Cette bactérie atténuée peut être utilisée en tant que vaccin vivant. De manière plus spécifique la bactérie peut être i(%Neisseria% %meningitidis%).

3/3,AB/33 (Item 8 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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00326885

DRUG FOR THE PREVENTION AND TREATMENT OF AUTO-IMMUNE AND VIRAL DISEASES,

AND DIAGNOSTIC AGENTS FOR DETECTING SAID DISEASES

MEDICAMENT DESTINE A LA PROPHYLAXIE ET AU TRAITEMENT DE MALADIES

AUTO-IMMUNES ET VIRALES, AGENTS DE DIAGNOSTIC POUR LE DEPISTAGE

DESDITES MALADIES

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Patent and Priority Information (Country, Number, Date):  
Patent: WO 9609395 A2 19960328  
Application: WO 95EP3726 19950921 (PCT/WO EP9503726)  
Priority Application: DE 4433708 19940921  
Designated States: AU CA JP US AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT  
SE  
Publication Language: German  
Fulltext Word Count: 24171

#### English Abstract

The present invention concerne drugs and diagnostic agents as well as diagnostic, therapeutic and preventive methods for treating auto-immune and viral diseases in humans, these diseases being caused by pathogenic bacteria which are, in particular, micro-organisms colonizing human mucus membranes and secreting given exoproteins which display structural similarities to human proteins. Proteins similar to IgA protease which are absorbed particularly well by cells and present as antigens on MHC molecules are of particular significance in this respect. The IgA protease polyprotein (IPP) of pathogenic *Neisseriae* has a particularly marked homology to human proteins. For example, a given IPP peptide has marked homology to the articular proteins link and aggrecan. It is thus proven, for example, that the IPP is an etiological agent of rheumatoid arthritis (RA). The auto-immune reaction is further encouraged by other properties of the IPP-producing *Neisseriae* and IPPs. A particularly important property is the ability of the IPP to activate viruses and viral elements. This concerns in particular the activation of proviral retroviruses and endogenic retroviruses in humans. Further auto-immune reactions are induced in humans owing to the activation of viruses and viral elements. The development of acquired immune deficiency syndrome (AIDS) is also explained by the IPP-dependent activation of the HIV provirus. The properties according to the invention of the pathogenic *Neisseriae* and the IPPs formed thereby give rise to numerous novel diagnostic, therapeutic and preventive processes.

#### French Abstract

La presente invention concerne des medicaments et des agents de diagnostic, ainsi que des procedes diagnostiques, therapeutiques et prophylactiques pour le traitement de maladies auto-immunes et virales chez l'homme, lesdites maladies pouvant etre causees par des bacteries pathogenes. Ces bacteries sont, en particulier, des micro-organismes qui colonisent les muqueuses de l'homme et secretent certaines exoproteines presentant des similitudes structurelles avec les proteines humaines. Les proteines similaires a la protease IgA, qui sont particulierement bien absorbees par les cellules et se presentent sous forme d'antigenes sur les molecules de CMH, ont une importance particuliere dans ce contexte. La polyproteine de la protease IgA (IPP) de *neisseria* pathogenes presente une homologie particulierement marquee avec les proteines humaines. Par exemple, un peptide determine de l'IPP presente une homologie marquee avec les proteines articulaires de liaison et Aggrecan. Il est donc prouve, par exemple, que l'IPP est un agent etiological de la polyarthrite rhumatoide (RA). La reaction auto-immune est en outre favorisee par d'autres proprietes des *neisseria* produisant l'IPP et des IPP. L'aptitude de l'IPP a activer les virus et les elements viraux constitue une propriete importante. Cela concerne en particulier l'activation de retrovirus proviraux et de retrovirus endogenes chez l'homme. D'autres reactions auto-immunes chez l'homme sont induites par l'activation de virus et d'elements viraux. En outre, le developpement du syndrome d'immunodeficiency acquise (SIDA) s'explique egalement par l'activite du provirus VIH dependant de l'IPP. Les proprietes, decrites dans l'invention, des *neisseria* pathogenes et des IPP ainsi formees, permettent de developper de nombreux procedes diagnostiques, therapeutiques et prophylactiques nouveaux.

0233293 DBR Accession No.: 99-03394 PATENT

New attenuated bacterium containing a modified %fur% %gene% - live, attenuated %Neisseria% %meningitidis% or Neisseria gonorrhoeae preparation; ferric uptake regulation gene mutation for use as human infection vaccine

AUTHOR: Baldwin T J; Borriello S P; Palmer H M

CORPORATE SOURCE: London, UK.

PATENT ASSIGNEE: Med.Res.Counc. 1998

PATENT NUMBER: WO 9856901 PATENT DATE: 981217 WPI ACCESSION NO.:

99-080894 (9907)

PRIORITY APPLIC. NO.: GB 9711964 APPLIC. DATE: 970609

NATIONAL APPLIC. NO.: WO 98GB1683 APPLIC. DATE: 980609

LANGUAGE: English

ABSTRACT: A new attenuated bacterium contains a modified ferric uptake regulation (%fur%) %gene%, where the expressed product is regulated independently of iron concentration in the environment of the bacterium. Also claimed are: a %Neisseria% %meningitidis% strain having genotype aroB (or aroL) lac:fur fusion, recA or aroL (or aroB), galE, lac:fusion, recA; a preparation of membrane vesicles obtained from the bacterium; and a method for the preparation of the new bacterium. The bacterium may also be Neisseria gonorrhoeae and may be used to protect individuals against bacterial infection, e.g. meningococcal meningitis, stomach ulcers, gastric infections, whooping cough, and infection in an individual with cystic fibrosis. The bacterium also forms the basis of a method for preparing vaccines. Changing the regulation of the %fur% %gene% increases expression of important protective antigens during bacterial growth, which increases the efficiency of live vaccines administered to humans or animals. (49pp)

app 10/13

3/3,AB/35 (Item 2 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

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0220831 DBR Accession Number: 98-02428

Genetic and physiological characterization of the %fur% %gene% of Pseudomonas sp. KC - encoding carbon tetrachloride degradation (conference abstract)

AUTHOR: Knaebel D B; Lewis T A; Austin P R; Crawford R L

CORPORATE AFFILIATE: Univ.Clarkson Univ.Idaho

CORPORATE SOURCE: Clarkson University, Potsdam, NY 13699-5715, USA.

JOURNAL: Abstr.Gen.Meet.Am.Soc.Microbiol. (97 Meet., 354) 1997

ISSN: 0067-2777 CODEN: 0005P

CONFERENCE PROCEEDINGS: American Society for Microbiology, 97th General Meeting, Miami Beach, FL, 4-8 May, 1997.

LANGUAGE: English

ABSTRACT: Pseudomonas sp. KC is capable of carbon tetrachloride degradation to carbon dioxide with little production of chloroform. This ability appears to be related to iron and cobalt availability. The activity of the iron regulatory element Fur was studied so that information obtained could be used to understand the carbon tetrachloride degrading activity of Pseudomonas sp. KC. Polymerase chain reaction was used to amplify the coding region of the %fur% %gene% of Pseudomonas sp. KC. This was cloned into plasmid pBluescript SK+ and sequenced. It had a high degree of DNA sequence similarity to Pseudomonas aeruginosa (84%), Pseudomonas putida (81%), Bordetella pertussis (66%), Vibrio cholerae (65%) and Neisseria gonorrhoea and %Neisseria% %meningitidis% (both 63%). Based on presumptive amino acid sequences, the Pseudomonas sp. KC Fur showed 93% identity to P. putida Fur and 90% identity to P. aeruginosa Fur. The cloned Pseudomonas sp. KC fur was able to complement the Fur-Escherichia coli SBC796. It also produced a protein that cross-reacted with anti E. coli Fur antibody. (0 ref)

3/3,AB/36 (Item 1 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

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04274010 H.W. WILSON RECORD NUMBER: BGSA00024010  
Iron metabolism in pathogenic bacteria.  
Ratledge, Colin  
Dover, Lynn G  
Annual Review of Microbiology v. 54 (2000) p. 881-941  
SPECIAL FEATURES: bibl diag tab ISSN: 0066-4227  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 29223

ABSTRACT: The ability of pathogens to obtain iron from transferrins, ferritin, hemoglobin, and other iron-containing proteins of their host is central to whether they live or die. To combat invading bacteria, animals go into an iron-withholding mode and also use a protein (Nramp1) to generate reactive oxygen species in an attempt to kill the pathogens. Some invading bacteria respond by producing specific iron chelators--siderophores--that remove the iron from the host sources. Other bacteria rely on direct contact with host iron proteins, either abstracting the iron at their surface or, as with heme, taking it up into the cytoplasm. The expression of a large number of genes (>40 in some cases) is directly controlled by the prevailing intracellular concentration of Fe(II) via its complexing to a regulatory protein (the Fur protein or equivalent). In this way, the biochemistry of the bacterial cell can accommodate the challenges from the host. Agents that interfere with bacterial iron metabolism may prove extremely valuable for chemotherapy of diseases. Reprinted by permission of the publisher.

3/3,AB/37 (Item 2 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04050514 H.W. WILSON RECORD NUMBER: BGSA99050514  
Contributions of genome sequencing to understanding the biology of  
*Helicobacter pylori*.  
AUGMENTED TITLE: review  
Ge, Zhongming  
Taylor, Diane E  
Annual Review of Microbiology v. 53 (1999) p. 353-87  
SPECIAL FEATURES: bibl il ISSN: 0066-4227  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 15698

ABSTRACT: About half of the world's population carries *Helicobacter pylori*, a gram-negative, spiral bacterium that colonizes the human stomach. The link between *H. pylori* and, ulceration as well as its association with the development of both gastric cancer and mucosa-associated lymphoid tissue lymphoma in humans is a serious public health concern. The publication of the genome sequences of two stains of *H. pylori* gives rise to direct evidence on the genetic diversity reported previously with respect to gene organization and nucleotide variability from strain to strain. The genome size of *H. pylori* strain 26695 is 1,6697,867 bp and is 1,643,831 bp for strain J99. Approximately 89% of the predicted open reading frames are common to both of the strains, confirming *H. pylori* as a single species. A region containing {similar}45% of *H. pylori* strain-specific open reading frames, termed the plasticity zone, is present on the chromosomes, verifying that some strain variability exists. Frequent alteration of nucleotides in the third position of the triplet codons and various copies of insertion elements on the individual chromosomes appear to contribute to distinct polymorphic fingerprints among strains analyzed by restriction fragment length polymorphisms, random amplified polymorphic DNA method, and repetitive element-polymerase chain reaction. Disordered chromosomal locations of some genes seen by pulsed-field gel electrophoresis are likely caused by rearrangement or inversion of certain segments in the genomes. Cloning and functional characterization of the genes involved in acidic survival, vacuolating toxin, cag-pathogenicity island, motility, attachment to epithelial cells, natural transformation, and the biosynthesis of lipopolysaccharides have considerably increased our



understanding of the molecular genetic basis for the pathogenesis of H. pylori. The homopolymeric nucleotide tracts and dinucleotide repeats, which potentially regulate the on- and off-status of the target genes by the strand-slipped mispairing mechanism, are often found in the genes encoding the outer-membrane proteins, in enzymes for lipopolysaccharide synthesis, and within DNA modification/restriction systems. Therefore, these genes may be involved in the H. pylori-host interaction. Reprinted by permission of the publisher.

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3/3,AB/38 (Item 1 from file: 16)  
DIALOG(R)File 16:Gale Group PROMT(R)  
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08927282 Supplier Number: 77416504  
PART II Prescription for success.(pharmaceuticals in  
development)(Illustration)  
News, Med Ad  
Med Ad News, v20, n7, pNA  
July, 2001  
Language: English Record Type: Fulltext  
Article Type: Illustration  
Document Type: Magazine/Journal; Trade  
Word Count: 34591

3/3,AB/39 (Item 1 from file: 135)  
DIALOG(R)File 135:NewsRx Weekly Reports  
(c) 2004 NewsRx. All rts. reserv.

0000115539 (USE FORMAT 7 OR 9 FOR FULLTEXT)  
Iron-responsive regulator fur not essential in  
Biotech Week, December 10, 2003, p.119

DOCUMENT TYPE: Expanded Reporting LANGUAGE: English  
RECORD TYPE: FULLTEXT  
WORD COUNT: 315  
?

Set	Items	Description
S1	57166	NEISSERIA (1W) MENINGITIDIS
S2	60	S1 AND FUR (1W) GENE
S3	39	RD (unique items)

? s s3 not py>1997

>>>One or more prefixes are unsupported

>>> or undefined in one or more files.

Processing

Processed 10 of 60 files ...

Processing

Processed 20 of 60 files ...

Processing

Processing

Processed 30 of 60 files ...

Processing

Processed 40 of 60 files ...

Processing

Completed processing all files

39 S3

108100699 PY>1997

S4 15 S3 NOT PY>1997

? t s4/3,ab/1-4

>>>No matching display code(s) found in file(s): 65, 107, 128-129, 135, 229, 342, 345, 398, 429, 446-447, 449, 459, 761

4/3,AB/1 (Item 1 from file: 73)

DIALOG(R)File 73:EMBASE

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05724381 EMBASE No: 1994118985

Cloning and sequence analysis of the %fur% %gene% encoding an iron-regulatory protein of %Neisseria% %meningitidis%

Karkhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.

Depart. Microbiol./Infectect. Dis., Univ. Calgary Hlth Sciences Center,

3330 Hospital Drive N.W., Calgary, Alta. T2N 4N1 Canada

Gene ( GENE ) (Netherlands) 1994, 141/1 (139-140)

CODEN: GENED ISSN: 0378-1119

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The %fur% %gene%, encoding an iron-regulatory protein in %Neisseria% %meningitidis% strain B16B6, has been cloned and sequenced. Its product showed a high degree of homology to known Fur sequences.

4/3,AB/2 (Item 1 from file: 440)

DIALOG(R)File 440:Current Contents Search(R)

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05728818 References: 39

TITLE: IDENTIFICATION, CLONING, AND SEQUENCING OF A GENE REQUIRED FOR FERRIC VIBRIOBACTIN UTILIZATION BY VIBRIO CHOLERAEE

AUTHOR(S): BUTTERTON JR; CALDERWOOD SB (Reprint)

CORPORATE SOURCE: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114

(Reprint); MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114;

HARVARD UNIV,SCH MED,DEPT MICROBIOL & MOLEC GENET/BOSTON//MA/02115

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N18 (SEP), P5631-5638

GENUINE ARTICLE#: PF222

ISSN: 0021-9193

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Chromosomal DNA downstream of the *Vibrio cholerae* ferric vibriobactin receptor gene, *viuA*, was cloned and sequenced, revealing an 813-bp open reading frame encoding a deduced protein of 271 amino acids. In vitro transcription-translation of this DNA confirmed expression of a protein of the expected size. A deletion mutation of this gene, *viuB*, was created in the classical *V. cholerae* strain O395 by in vivo marker exchange. By cross-feeding studies, this mutant was unable to utilize

exogenous ferric vibriobactin but synthesized the siderophore normally; synthesis of siderophore by the mutant was also confirmed by the Arnow assay. Complementation of the mutant with a plasmid encoding only *viuB* restored ferric vibriobactin utilization to normal. Unexpectedly, hydropathicity analysis of *ViuB* did not reveal a signal sequence or transmembrane domain, suggesting that *ViuB* is not a periplasmic or membrane protein but may be a cytoplasmic protein involved in ferric vibriobactin uptake and processing, perhaps analogous to the *Escherichia coli* protein *Fes*. *ViuB* was not, however, homologous to *Fes* or to other proteins in the database. Complementation studies revealed that the cloned *V. cholerae viuB* gene could complement an *E. coli fes* mutant but that the cloned *E. coli fes* gene could not complement a *V. cholerae viuB* mutant; Northern (RNA) blot analysis of RNA from wild-type *V. cholerae* grown in high- and low-iron media revealed a monocistronic *viuB* message that was negatively regulated by iron at the transcriptional level. The promoter of *viuB* was located by primer extension and contained a nucleotide sequence highly homologous to the *E. coli Fur* binding consensus sequence, suggesting that expression of *viuB* is under the control of the *V. cholerae fur* gene.

4/3,AB/3 (Item 2 from file: 440)  
DIALOG(R)File 440:Current Contents Search(R)  
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05468121 References: 44

TITLE: CHARACTERIZATION OF THE VIBRIO CHOLERAЕ OUTER MEMBRANE HEME

TRANSPORT PROTEIN HUTA - SEQUENCE OF THE GENE, REGULATION OF

EXPRESSION, AND HOMOLOGY TO THE FAMILY OF TONB-DEPENDENT PROTEINS

AUTHOR(S): HENDERSON DP; PAYNE SM (Reprint)

CORPORATE SOURCE: UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712 (Reprint);

UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N11 (JUN), P3269-3277

GENUINE ARTICLE#: NN851

ISSN: 0021-9193

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The regulation of *hutA*, the *Vibrio cholerae* gene encoding a 77-kDa iron-regulated outer membrane protein required for heme iron utilization, was characterized, and the DNA sequence of the gene was determined. A *hutA::Tn5 lac* fusion generated previously (D. P. Henderson and S. M. Payne, *Mol. Microbiol.* 7:461-469, 1993) was transformed into *Fur(-)* and *Fur(+)* strains of *Escherichia coli* and *V. cholerae*. The results of beta-galactosidase assays on the transformed strains demonstrated that transcription of *hutA* is regulated by the *Fur* repressor protein in *E. coli* and at least partially regulated by *Fur* in *V. cholerae*. Analysis of the DNA sequence of *hutA* indicated that a sequence homologous to the *E. coli* consensus *Fur* box was present in the promoter region of *hutA*. The amino acid sequence of *HutA* is homologous to those of several TonB-dependent outer membrane proteins. However, when the *V. cholerae* heme utilization system, which requires one or more genes encoded by the recombinant plasmid *pHUT10* in addition to *hutA* Carried on a second vector, was transferred to a wild-type strain and an isogenic *tonB* mutant of *E. coli*, the *tonB* mutant could utilize heme iron as efficiently as the wild-type strain. These data indicate that the *V. cholerae* heme utilization system reconstituted in *E. coli* does not require a functional TonB protein. The *tonB* mutant transformed with the heme utilization plasmids could not utilize the siderophore ferrichrome as an iron source, indicating that none of the genes encoded on the heme utilization plasmids complements the *tonB* defect in *E. coli*. It is possible that a gene(s) encoded by the recombinant heme utilization plasmids encodes a protein serving a TonB-like function in *V. cholerae*. A region in the carboxy terminus of *HutA* is homologous to the horse hemoglobin zeta chain, and the amino acids involved in forming the heme pocket in the zeta chain are conserved in *HutA*. These data suggest that this region of *HutA* is involved in heme binding.

4/3,AB/4 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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05375535 Genuine Article#: VU635 Number of References: 43

Title: IDENTIFICATION AND PURIFICATION OF A HEMOGLOBIN-BINDING

OUTER-MEMBRANE PROTEIN FROM NEISSERIA-GONORRHOEAE (Abstract Available)

Author(s): CHEN CJ; SPARLING PF; LEWIS LA; DYER DW; ELKINS C

Corporate Source: UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599;

UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV

OKLAHOMA,HLTH SCI CTR,DEPT MICROBIOL & IMMUNOL/OKLAHOMA CITY//OK/73190

Journal: INFECTION AND IMMUNITY, 1996, V64, N12 (DEC), P5008-5014

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ISSN: 0019-9567

Language: ENGLISH Document Type: ARTICLE

Abstract: The majority of in vitro-grown *Neisseria gonorrhoeae* strains were unable to use hemoglobin as the sole source of iron for growth (Hgb(-)), but a minor population was able to do so (Hgb(+)). The ability of Hgb(+) gonococci to utilize hemoglobin as the iron source was associated with the expression of an iron-repressible 89-kDa hemoglobin-binding protein in the outer membrane. The N-terminal amino acid sequence of this protein revealed amino acids, from positions 2 to 16, identical to those of HpuB, an 85 kDa iron-regulated hemoglobin-haptoglobin utilization outer membrane protein of *Neisseria meningitidis*. Isogenic mutants constructed by allelic replacement with a meningococcal hpu::mini-Tn3erm construct no longer expressed the 89-kDa protein. Mutants could not utilize hemoglobin to support growth but still grew on heme. Thus, the gonococcal HpuB homolog is a functional hemoglobin receptor and is essential for growth with hemoglobin.

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 **PALM INTRANET**Day : Tuesday  
Date: 3/2/2004  
Time: 13:42:30

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